

SEQUENCE LISTING

<110> Jin-Town Wang

Tzu-Lung Lin

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<160>5

<170>MICROSOFT WORD 2000

<210>SEQ ID NO:1

<211>LENGTH:5

<212>DNA

<213>ORGANISM: *Helicobacter pylori*

<400>SEQUENCE:1

ccatc 5

<210>SEQ ID NO:2

<211>LENGTH:1617

<212> DNA

<213> ORGANISM: *Helicobacter pylori*

<300>

<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

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ata	atc	atg	caa	att	atc	aaa	tcc	gtt	ttg	gct	cat	agg	ctt	tat	aga	cct	act	tct	ctc	180
aat	caa	aat	aaa	gaa	ttg	aaa	gaa	aaa	ttt	gac	tcc	aat	gaa	tat	gtc	ttt	agc	gat	gaa	240
gag	tta	gaa	cgc	att	ata	gaa	ata	tcc	cca	caa	aat	cat	aaa	gaa	atg	ggc	ttt	gag	cat	300

gga	tgg	gaa	agc	cgg	ttt	gac	act	tgg	tat	aag	ctt	atg	tgt	gag	ttt	ggt	ttt	tgc	tac	360
tat	gca	aaa	tat	gag	aaa	ata	ctc	atc	agc	gat	agc	gct	aag	atg	ctt	att	ctt	gct	tat	420
tac	aat	aaa	gaa	aac	gat	gct	ttt	aaa	gaa	agc	gtt	gat	gaa	agc	gta	gtt	ggg	gct	ata	480
ttt	tta	aac	gct	ctg	tct	aaa	tat	gaa	gta	gga	aac	cct	tac	aaa	aag	aat	tta	aac	cat	540
aac	aac	cct	tcc	aaa	cta	ttg	ctc	tcg	ctt	tta	aaa	cga	ctc	aaa	aat	gcc	cat	cta	acc	600
ccc	cta	tct	gtc	aaa	gaa	atc	cct	att	tta	ctt	tgt	tgg	aaa	gac	gat	aac	gct	aat	ggg	660
ctt	tat	gac	tac	att	att	cgt	tta	aga	caa	gaa	atc	gtt	act	atc	aat	aaa	aca	gaa	tcc	720
agc	tac	tca	gat	gaa	ttt	atc	tat	gaa	aaa	tgc	cta	aaa	ctt	tta	gaa	agt	gtt	aat	aaa	780
aca	cga	ttt	aaa	atg	agc	caa	atc	act	aac	gaa	gcc	gtt	gat	gaa	tac	att	aga	aaa	atg	840
cgt	att	aca	gga	ctt	att	tca	ttg	cgt	ggt	aat	ggt	agg	ttt	att	gat	att	aat	act	aat	900
gaa	aat	aat	aaa	ata	gat	tac	att	tta	caa	acc	cat	aag	gct	ttt	aaa	ggg	gat	tat	tta	960
aac	gac	act	caa	gct	aac	aaa	ctc	gcc	ttt	ttt	aac	tac	atg	gcg	atc	gtg	gat	agc	ttt	1020
ctt	gtt	agt	gtt	act	cca	atc	agc	gct	aat	gag	agc	gtt	aaa	tca	agc	aaa	ttg	aat	gaa	1080
cta	gca	aac	act	tat	act	aaa	gat	ttt	atc	aag	caa	tta	ctc	att	act	tgt	aac	aag	1140	
caa	gaa	tca	aaa	gat	agt	ttt	tta	aga	ctc	att	gat	aaa	cct	tta	cgc	tta	gaa	ttt	tta	1200
agc	gct	att	tcc	ttg	aaa	caa	cat	ttt	gaa	aat	tta	agc	gtg	ata	ccc	aat	tat	aaa	agc	1260
gat	gat	gaa	ggc	ttg	ccc	gta	tac	aca	gca	agc	ggt	aat	aaa	cct	gat	att	gta	gct	atg	1320
gac	aca	aaa	gcc	caa	agt	tat	ata	gaa	gtg	agc	ttg	att	aga	gac	aga	agt	caa	agt	acc	1380
ttg	gaa	atg	ata	cct	att	gcc	aga	cat	tta	aaa	gaa	ttg	att	aaa	aat	agc	acc	gat	att	1440
aga	gaa	aaa	ttt	agt	gtt	ttt	gta	gct	cca	aat	atc	cat	gat	gat	gcc	aaa	gaa	tat	gcg	1500
gaa	ttt	gcc	caa	tcc	aaa	gac	aat	att	aat	ata	tgt	tgt	tat	gct	att	aat	gat	ttt	atc	1560
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<210> SEQ ID NO:3

<211> LENGTH:538

<212> PRT

<213> ORGANISM: *Helicobacter pylori*

<400> SEQUENCE:3

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 20 25 30

Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
 35 40 45

Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
 50 55 60

Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
 65 70 75 80

Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
 85 90 95

Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
 100 105 110

Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
 115 120 125

Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
 130 135 140

Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
 145 150 155 160

Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
 165 170 175

Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
 180 185 190

Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
 195 200 205

Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
 210 215 220

Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe
 225 230 235 240

Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
 245 250 255

Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
 260 265 270

Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
 275 280 285

Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
 290 295 300

Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
 305 310 315 320

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				340				345					350		
Val	Lys	Ser	Ser	Lys	Leu	Asn	Glu	Leu	Ala	Asn	Thr	Tyr	Thr	Lys	Asp
				355				360				365			
Phe	Ile	Lys	Gln	Glu	Leu	Leu	Ile	Thr	Cys	Asn	Lys	Gln	Glu	Ser	Lys
				370			375				380				
Asp	Ser	Phe	Leu	Arg	Leu	Ile	Asp	Lys	Pro	Leu	Arg	Leu	Glu	Phe	Leu
				385			390			395			400		
Ser	Ala	Ile	Phe	Leu	Lys	Gln	His	Phe	Glu	Asn	Leu	Ser	Val	Ile	Pro
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Asn	Tyr	Lys	Ser	Asp	Asp	Glu	Gly	Leu	Pro	Val	Tyr	Thr	Ala	Ser	Gly
				420			425					430			
Asn	Lys	Pro	Asp	Ile	Val	Ala	Met	Asp	Thr	Lys	Ala	Gln	Ser	Tyr	Ile
				435			440					445			
Glu	Val	Ser	Leu	Ile	Arg	Asp	Arg	Ser	Gln	Ser	Thr	Leu	Glu	Met	Ile
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Pro	Ile	Ala	Arg	His	Leu	Lys	Glu	Leu	Ile	Lys	Asn	Ser	Thr	Asp	Ile
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Arg	Glu	Lys	Phe	Ser	Val	Phe	Val	Ala	Pro	Asn	Ile	His	Asp	Asp	Ala
				485			490					495			
Lys	Glu	Tyr	Ala	Glu	Phe	Ala	Gln	Phe	Lys	Asp	Asn	Ile	Asn	Ile	Cys
				500			505					510			
Cys	Tyr	Ala	Ile	Asn	Asp	Phe	Ile	Lys	Lys	Val	Glu	Asn	Ser	Ile	Glu
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<211>780

<212> DNA

<213> ORGANISM: *Helicobacter pylori*

<300>

<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

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gat	tgt	gtc	aaa	atc	ggt	agc	att	aga	gag	cat	ata	gaa	agc	tta	aac	tta	gat	aaa	tta	180
aat	aaa	gat	att	tta	tta	aca	agc	ctg	att	tat	tca	atg	gat	aag	ata	gct	aac	acg	gta	240
ggg	cat	tat	gaa	gct	tat	agg	aaa	aaa	gag	att	ttg	caa	gat	aga	ttt	att	ttt	gag	ctt	300
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agc	cgg	ttt	tat	cat	ctc	tat	gaa	aac	cta	gtg	cag	tgg	aaa	aaa	ccc	aaa	ctc	tat	gga	480
aca	gct	tta	aag	cca	tca	tgc	gag	aac	atg	agc	gaa	tat	tgc	cgc	tct	aat	gcc	aag	aaa	540
gaa	ttg	agc	gat	tta	att	gaa	aaa	cta	gat	tgt	aaa	agg	att	gct	tta	act	tat	aat	aat	600
acc	tat	aac	tct	aag	tct	agc	tct	tcg	caa	aat	aaa	ata	ggc	ttt	aaa	gat	tta	gtg	gaa	660
att	ttg	agt	caa	aaa	gga	aaa	tta	agc	gtt	aaa	gaa	aag	gct	cat	agt	ttt	ttt	aat	tca	720
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<210>SEQ ID NO:5

<211>LENGTH:846

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<213> ORGANISM: *Helicobacter pylori*

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<308>DDBJ/EMBL/Genbank : Accession No. : AB118944

<400>SEQUENCE:5

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act	aat	att	atc	aat	tta	cat	aaa	act	tta	agc	aag	ttc	aat	gtt	tgt	gag	ctt	ttt	gat	180
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cct	gtg	ggt	aat	gtg	gat	ttc	aat	gaa	aat	gtt	tat	aat	gcc	cta	aaa	aac	tac	ata	gat	480
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cta	gat	aaa	aag	gga	gtt	tta	ttt	ggt	ata	act	aat	ctt	att	tat	cac	aag	gga	gag	act	720
aat	ttt	att	tta	aaa	gaa	tgg	gct	aaa	aaa	tat	tat	att	ttt	aat	atc	aaa	agt	aat	tat	780
atc	agt	tat	aat	gac	aat	act	att	aaa	gaa	gat	agt	caa	gaa	atc	ttt	gta	act	aat	tat	840
agg	tga																			846